



SEQUENCE LISTING

<110> Bramberg, Richard

<120> Methods of Inhibiting Inflammation

<130> 18989-033

<140> 10/808,052

<141> 2004-03-24

<150> 60/457,048

<151> 2003-03-24

<160> 16

<170> PatentIn Ver. 2.1

<210> 1

<211> 21

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chemically synthesized siRNA

<400> 1

aagcucugga acuaccaacg a

21

<210> 2

<211> 21

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chemically synthesized siRNA

<400> 2

ucguugguag uuccagagcu u

21

<210> 3

<211> 3392

<212> DNA

<213> Homo sapiens

<400> 3

```
actccctcac tggctgccat tgaaagagtc cacttctcag tgactcctag ctgggcactg 60
gatgcagttg aggattgctg gtcaatatga ttcttcttgc tgtgcttttt ctctgcttca 120
tttcctcata ttcagcttct gttaaagggtc acacaactgg tctctcatta aataatgacc 180
ggctgtacaa gctcacgtac tccactgaag ttcttcttga tcggggcaaa ggaaaactgc 240
aagacagcgt gggctaccgc atttctctca acgtggatgt ggccttacta tggaggaatc 300
ctgatggtga tgatgaccag ttgatccaaa taacgatgaa ggatgtaaat gttgaaaatg 360
tgaatcagca gagaggagag aagagcatct tcaaaggaaa aagcccatct aaaataatgg 420
gaaaggaaaa cttggaagct ctgcaaagac ctacgctcct tcattctaac catggaaagg 480
tcaaagagtt ctactcatat caaatgagg cagtggccat agaaaatatc aagagaggtc 540
tggtagcctt atttcagaca cagttaagct ctggaaccac caatgaggta gatattctctg 600
gaaattgtaa agtgacctac caggctcatc aagacaaagt gatcaaaatt aaggccttgg 660
attcatgcaa aatagcgagg tctggattta cgaccccaaa tcaggtcttg ggtgtcagtt 720
caaaagctac atctgtcacc acctataaga tagaagacag ctttggtata gctgtgcttg 780
ctgaagaaac acacaatttt ggactgaatt tcctacaaac cattaagggg aaaatagtat 840
```

```

cgaagcagaa attagagctg aagacaaccg aagcaggccc aagattgatg tctggaaagc 900
aggctgcagc cataatcaaa gcagttgatt caaagtacac ggccattccc attgtggggc 960
aggctctcca gagccactgt aaaggatgtc cttctctctc ggagctctgg cgggtccacca 1020
ggaaatacct gcagcctgac aacctttcca aggctgaggg tgtcagaaac ttcctggcct 1080
tcattcagca cctcaggact gcgaagaaag aagagatcct tcaaatacta aagatgggaa 1140
ataaggaagt attacctcag ctggtggatg ctgtcacctc tgctcagacc tcagactcat 1200
tagaagccat tttggacttt ttggatttca aaagtgcagc cagcattatc ctccaggaga 1260
ggtttctcta tgcctgtgga tttgcttctc atcccaatga agaactcctg agagccctca 1320
ttagtaagtt caaaggttct attggtagca gtgacatcag agaaactggt atgatcatca 1380
ctgggacact tgtcagaaag ttgtgtcaga atgaaggctg caaactcaaa gcagtagtgg 1440
aagctaagaa gttaatcctg ggaggacttg aaaaagcaga gaaaaaagag gacaccagga 1500
tgtatctgct ggctttgaag aatgccctgc ttccagaagg catcccaagt cttctgaagt 1560
atgcagaagc aggagaaggg cccatcagcc acctggctac cactgctctc cagagatatg 1620
atctcccttt cataactgat gaggtgaaga agaccttaaa cagaatatac caccaaaacc 1680
gtaaagttca tgaaaagact gtgcgcactg ctgcagctgc tatcatttta aataacaatc 1740
catcctacat ggacgtcaag aacatcctgc tgtctattgg ggagcttccc caagaaatga 1800
ataaatacat gctcgccatt gttcaagaca tcctacggtt ggaaatgcct gcaagcaaaa 1860
ttgtccgctc agttctgaag gaaatggctc ctcacaatta tgaccgtttc tccaggagtg 1920
gatcttcttc tgcctacact ggctacatag aacgtagtcc ccgttcggca tctacttaca 1980
gcctagacat tctctactcg ggttctggca ttctaaggag aagtaacctg aacatctttc 2040
agtacattgg gaaggctggg cttcacggta gccagggtgg tattgaagcc caaggactgg 2100
aagccttaat cgcagccacc cctgacgagg gggaggagaa ccttgactcc tatgctggta 2160
tgtcagccat cctctttgat gttcagttca gacctgtcac ctttttcaac ggatacagt 2220
atttgatgtc caaaatgtcg tcagcatctg gcgaccctat cagtgtgggt aaaggactta 2280
ttctgctaat agatcattct caggaacttc agttacaatc tggactaaaa gccaatatag 2340
agggtccaggg tgggtctagc attgatattt cagggtgcaat ggagtttagc ttgtgggtatc 2400
gtgagtctaa aacccgagtg aaaaataggg tgactgtggg aataaccact gacatcacag 2460
tggactcctc ttttgtgaaa gctggcctgg aaaccagtac agaaacagaa gcaggcttgg 2520
agtttatctc cacagtgcag tttctcagt acccattctt agtttgcag cagatggaca 2580
aggatgaagc tccattcagg caatttgaga aaaagtacga aaggctgtcc acaggcagag 2640
gttatgtctc tcagaaaaga aaagaaagcg tattagcagg atgtgaattc ccgctccatc 2700
aagagaactc agagatgtgc aaagtgggtg ttgcccctca gccggatagt acttccagcg 2760
gatgggtttg aaactgacct gtgatatttt acttgaattt gtctccccga aagggacaca 2820
atgtggcatg actaagtact tgctctctga gagcacagcg ttacatattt tacctgtatt 2880
taagattttt gtaaaaagct acaaaaaact gcagtttgat caaatttggg tatatgcagt 2940
atgtaccca cagcgtcatt ttgaatcatc atgtgacgct ttcaacaacg ttcttagttt 3000
acttatacct ctctcaaatc tcatttggtg cagtcagaat agttattctc taagaggaaa 3060
ctagtgtttg ttaaaaacaa aaataaaaac aaaccacac aaggagaacc caattttggt 3120
tcaacaattt ttgatcaatg tatatgaagc tcttgatagg acttccttaa gcatgacggg 3180
aaaaccaaac acgttcccta atcaggaaaa aaaaaaaata aaaaaagtaa gacacaaaac 3240
aaccattttt ttctcttttt ttggagttgg gggcccaggg agaagggaca aggcctttta 3300
aagacttggt agccaacttc aagaattaat atttatgtct ctgttattgt tagttttaag 3360
ccttaaggta gaaggcacat agaaataaca tc 3392

```

<210> 4
 <211> 894
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Ile Leu Leu Ala Val Leu Phe Leu Cys Phe Ile Ser Ser Tyr Ser
 1 5 10 15
 Ala Ser Val Lys Gly His Thr Thr Gly Leu Ser Leu Asn Asn Asp Arg
 20 25 30
 Leu Tyr Lys Leu Thr Tyr Ser Thr Glu Val Leu Leu Asp Arg Gly Lys
 35 40 45
 Gly Lys Leu Gln Asp Ser Val Gly Tyr Arg Ile Ser Ser Asn Val Asp
 50 55 60
 Val Ala Leu Leu Trp Arg Asn Pro Asp Gly Asp Asp Asp Gln Leu Ile

65	70	75	80
Gln Ile Thr Met Lys Asp Val Asn Val Glu Asn Val Asn Gln Gln Arg	85	90	95
Gly Glu Lys Ser Ile Phe Lys Gly Lys Ser Pro Ser Lys Ile Met Gly	100	105	110
Lys Glu Asn Leu Glu Ala Leu Gln Arg Pro Thr Leu Leu His Leu Ile	115	120	125
His Gly Lys Val Lys Glu Phe Tyr Ser Tyr Gln Asn Glu Ala Val Ala	130	135	140
Ile Glu Asn Ile Lys Arg Gly Leu Ala Ser Leu Phe Gln Thr Gln Leu	145	150	155
Ser Ser Gly Thr Thr Asn Glu Val Asp Ile Ser Gly Asn Cys Lys Val	165	170	175
Thr Tyr Gln Ala His Gln Asp Lys Val Ile Lys Ile Lys Ala Leu Asp	180	185	190
Ser Cys Lys Ile Ala Arg Ser Gly Phe Thr Thr Pro Asn Gln Val Leu	195	200	205
Gly Val Ser Ser Lys Ala Thr Ser Val Thr Thr Tyr Lys Ile Glu Asp	210	215	220
Ser Phe Val Ile Ala Val Leu Ala Glu Glu Thr His Asn Phe Gly Leu	225	230	235
Asn Phe Leu Gln Thr Ile Lys Gly Lys Ile Val Ser Lys Gln Lys Leu	245	250	255
Glu Leu Lys Thr Thr Glu Ala Gly Pro Arg Leu Met Ser Gly Lys Gln	260	265	270
Ala Ala Ala Ile Ile Lys Ala Val Asp Ser Lys Tyr Thr Ala Ile Pro	275	280	285
Ile Val Gly Gln Val Phe Gln Ser His Cys Lys Gly Cys Pro Ser Leu	290	295	300
Ser Glu Leu Trp Arg Ser Thr Arg Lys Tyr Leu Gln Pro Asp Asn Leu	305	310	315
Ser Lys Ala Glu Ala Val Arg Asn Phe Leu Ala Phe Ile Gln His Leu	325	330	335
Arg Thr Ala Lys Lys Glu Glu Ile Leu Gln Ile Leu Lys Met Glu Asn	340	345	350
Lys Glu Val Leu Pro Gln Leu Val Asp Ala Val Thr Ser Ala Gln Thr	355	360	365
Ser Asp Ser Leu Glu Ala Ile Leu Asp Phe Leu Asp Phe Lys Ser Asp	370	375	380
Ser Ser Ile Ile Leu Gln Glu Arg Phe Leu Tyr Ala Cys Gly Phe Ala	385	390	395
Ser His Pro Asn Glu Glu Leu Leu Arg Ala Leu Ile Ser Lys Phe Lys	405	410	415

Gly Ser Ile Gly Ser Ser Asp Ile Arg Glu Thr Val Met Ile Ile Thr
 420 425 430
 Gly Thr Leu Val Arg Lys Leu Cys Gln Asn Glu Gly Cys Lys Leu Lys
 435 440 445
 Ala Val Val Glu Ala Lys Lys Leu Ile Leu Gly Gly Leu Glu Lys Ala
 450 455 460
 Glu Lys Lys Glu Asp Thr Arg Met Tyr Leu Leu Ala Leu Lys Asn Ala
 465 470 475 480
 Leu Leu Pro Glu Gly Ile Pro Ser Leu Leu Lys Tyr Ala Glu Ala Gly
 485 490 495
 Glu Gly Pro Ile Ser His Leu Ala Thr Thr Ala Leu Gln Arg Tyr Asp
 500 505 510
 Leu Pro Phe Ile Thr Asp Glu Val Lys Lys Thr Leu Asn Arg Ile Tyr
 515 520 525
 His Gln Asn Arg Lys Val His Glu Lys Thr Val Arg Thr Ala Ala Ala
 530 535 540
 Ala Ile Ile Leu Asn Asn Asn Pro Ser Tyr Met Asp Val Lys Asn Ile
 545 550 555 560
 Leu Leu Ser Ile Gly Glu Leu Pro Gln Glu Met Asn Lys Tyr Met Leu
 565 570 575
 Ala Ile Val Gln Asp Ile Leu Arg Leu Glu Met Pro Ala Ser Lys Ile
 580 585 590
 Val Arg Arg Val Leu Lys Glu Met Val Ala His Asn Tyr Asp Arg Phe
 595 600 605
 Ser Arg Ser Gly Ser Ser Ser Ala Tyr Thr Gly Tyr Ile Glu Arg Ser
 610 615 620
 Pro Arg Ser Ala Ser Thr Tyr Ser Leu Asp Ile Leu Tyr Ser Gly Ser
 625 630 635 640
 Gly Ile Leu Arg Arg Ser Asn Leu Asn Ile Phe Gln Tyr Ile Gly Lys
 645 650 655
 Ala Gly Leu His Gly Ser Gln Val Val Ile Glu Ala Gln Gly Leu Glu
 660 665 670
 Ala Leu Ile Ala Ala Thr Pro Asp Glu Gly Glu Glu Asn Leu Asp Ser
 675 680 685
 Tyr Ala Gly Met Ser Ala Ile Leu Phe Asp Val Gln Leu Arg Pro Val
 690 695 700
 Thr Phe Phe Asn Gly Tyr Ser Asp Leu Met Ser Lys Met Leu Ser Ala
 705 710 715 720
 Ser Gly Asp Pro Ile Ser Val Val Lys Gly Leu Ile Leu Leu Ile Asp
 725 730 735
 His Ser Gln Glu Leu Gln Leu Gln Ser Gly Leu Lys Ala Asn Ile Glu
 740 745 750

Val Gln Gly Gly Leu Ala Ile Asp Ile Ser Gly Ala Met Glu Phe Ser
755 760 765

Leu Trp Tyr Arg Glu Ser Lys Thr Arg Val Lys Asn Arg Val Thr Val
770 775 780

Val Ile Thr Thr Asp Ile Thr Val Asp Ser Ser Phe Val Lys Ala Gly
785 790 795 800

Leu Glu Thr Ser Thr Glu Thr Glu Ala Gly Leu Glu Phe Ile Ser Thr
805 810 815

Val Gln Phe Ser Gln Tyr Pro Phe Leu Val Cys Met Gln Met Asp Lys
820 825 830

Asp Glu Ala Pro Phe Arg Gln Phe Glu Lys Lys Tyr Glu Arg Leu Ser
835 840 845

Thr Gly Arg Gly Tyr Val Ser Gln Lys Arg Lys Glu Ser Val Leu Ala
850 855 860

Gly Cys Glu Phe Pro Leu His Gln Glu Asn Ser Glu Met Cys Lys Val
865 870 875 880

Val Phe Ala Pro Gln Pro Asp Ser Thr Ser Ser Gly Trp Phe
885 890

<210> 5
<211> 2878
<212> DNA
<213> Mus musculus

<400> 5

ctggatgtgg	cagaggggagc	cagcatgatac	ctcttggcag	tgccttttct	ctgcttcttc	60
tcctcctact	ctgcttccgt	taaaggtcac	acaactggcc	tctcattaaa	taatgagcgg	120
ctatacaagc	tcacgtactc	cactgaagtg	tttcttgatg	ggggcaaagg	aaaaccgcaa	180
gacagcgtgg	gctacaaaat	ctcatctgat	gtggacgttg	tggtactgtg	gaggaatcct	240
gatggtgatg	atgatcaagt	gatccaagtc	acgataacag	ctgttaacgt	tgaaaatgcg	300
ggtcaacaga	gagggcgagaa	gagcatcttc	cagggcaaaa	gtacacctaa	gatcataggg	360
aaggacaacc	tgagggctct	gcagagaccc	atgcttcttc	atctgggtccg	ggggaaggtc	420
aaggagttct	actcctatga	aaacgagcca	gtgggcatag	aaaatctcaa	gagaggcttg	480
gctagcttat	tccagatgca	gctaagctct	ggaactacca	acgaggtaga	tatctctggg	540
gattgtaaag	tgacctacca	ggcccaacaa	gacaaagtgg	tcaaaattaa	ggctctggat	600
acatgcaaaa	ttgagcggtc	tggtatttaca	acggcaaac	aggtgctggg	cgtcagttca	660
aaagccacat	ctgtcactac	ctacaagata	gaggacagct	ttgtcaccgc	tgtgcttgca	720
gaagagacca	gggcttttgc	cttgaacttc	caacaaacca	tagcaggaaa	aatagtgtca	780
aagcagaaat	tggaagtga	gacaactgaa	gccggcccaa	ggatgatccc	cggaagcaa	840
gtggcagggtg	taattaaagc	agttgattcc	aaatacaaa	ccattcccat	tgtgggacag	900
gtcctcgagc	gtgtctgcaa	aggatgccct	tctctggcgg	agcactggaa	gtccatcaga	960
aagaacctgg	agcctgaaaa	cctgtccaag	gccgaggctg	tccagagctt	cctggccttc	1020
atccagcacc	tccggacttc	gaggagagaa	gagatcctcc	agattctgaa	ggcagagaag	1080
aaagaagtgc	tccctcagct	ggtggatgcc	gtcactctctg	ctcagactcc	agactcgcta	1140
gaagccatcc	tggacttttt	ggatttcaaa	agtgacagca	gtatcatact	ccaggaaagg	1200
ttcctctatg	cctgtggctt	tgccacccac	cctgatgaag	aactcctacg	agccctcctt	1260
agtaagtcca	aaggttcctt	tgcaagcaac	gacatcagag	agtcggttat	gatcatcatt	1320
ggagccctag	tcaggaagct	gtgtcagaat	gaaggctgca	agctcaaggc	agtggtggaa	1380
gctaagaagc	tgatcctggg	aggacttgaa	aaaccagaga	agaaagaaga	caccacaatg	1440
tacctgctgg	ccctgaagaa	tgcccttgctt	cccgaaggca	tcccgtcctt	tctgaagtat	1500
gctgagctg	gagaagggcc	cgtcagccac	ctggccacca	ctgttctcca	gagatacgat	1560
gtctccttca	tcacagatga	ggtgaagaag	accttgaaca	ggatatacca	ccagaatcgt	1620
aaggttcattg	agaagacggg	gcgcacaact	gccgctgctg	tcatcttaaa	gaacccatcc	1680
tacatggatg	tgaagaacat	cctgctgtcc	attggggaac	tcccgaagaa	gatgaacaaa	1740
tacatgctca	ccgttgtgca	agacatcctg	cattttgaaa	tgcttgcaag	caaatgatc	1800

```

cgctcgagttc tcaaggagat ggctgttcac aattatgacc gtttctccaa gagtggatcc 1860
tcttctgcct atactggcta cgtagaacgt agccccgtg cagcgtccac atacagcctt 1920
gacatccttt actctggctc tggcattctg aggagaagta acctgaacat cttccagtac 1980
atcaaaggaa cagagcttca tggtagtcag gtggtgattg aagcccaagg gctggaaggc 2040
ttaattgcag ccactcctga tgaaggagag gagaaccttg actcttatgc tggcatgtca 2100
gccatcctgt ttgatgttca gcttaggcct gtcacatttt ttaatggata cagtgatttg 2160
atgtccaaaa tgctgtcggc atccggcgac cctgtcagcg tggtgaaagg gcttattctg 2220
ttaatagacc attctcagga tattcagctg caatctggac taaaggccaa tatggagatc 2280
caggggtggc tagctattga tatttctggg tcaatggaat tcagtctgtg gtatcgcgag 2340
tctaaaaccc gagtgaaaaa tcgggtggct gtggtgataa ccagcgacgt cacagtggat 2400
gcctcttttg tgaaagctgg tctggaaagc agagcggaga cagaggctgg gctggagttc 2460
atctccacag tgcagttctc acagtaccg ttcttgggtc gcatgcagat ggacaaggct 2520
gaagccccac tcaggcaatt cgagacaaag tatgaaaggc tatctacagg caggggatat 2580
gtctctcgga gaagaaaaga gaggctagtg gccggatgtg aactccccct ccatcaacag 2640
aactctgaga tgtgcaacgt ggtattccca cctcagccag aaagcgataa ctccggtgga 2700
tggttttgat tcccgtgggt tcccttcac cagaacgata tgctatgacg tgctgaccc 2760
ttgctctctg agagcacagt gtttacatat ttacctgtat ttaagatgtt tgtaaagagc 2820
agtggagaac ttcagttgat taaagttgaa cctattcagg agaagacca cagtgtcc 2878

```

<210> 6
 <211> 894
 <212> PRT
 <213> Mus musculus

```

<400> 6
Met Ile Leu Leu Ala Val Leu Phe Leu Cys Phe Phe Ser Ser Tyr Ser
  1             5             10             15

Ala Ser Val Lys Gly His Thr Thr Gly Leu Ser Leu Asn Asn Glu Arg
      20             25             30

Leu Tyr Lys Leu Thr Tyr Ser Thr Glu Val Phe Leu Asp Gly Gly Lys
      35             40             45

Gly Lys Pro Gln Asp Ser Val Gly Tyr Lys Ile Ser Ser Asp Val Asp
      50             55             60

Val Val Leu Leu Trp Arg Asn Pro Asp Gly Asp Asp Asp Gln Val Ile
      65             70             75             80

Gln Val Thr Ile Thr Ala Val Asn Val Glu Asn Ala Gly Gln Gln Arg
      85             90             95

Gly Glu Lys Ser Ile Phe Gln Gly Lys Ser Thr Pro Lys Ile Ile Gly
      100            105            110

Lys Asp Asn Leu Glu Ala Leu Gln Arg Pro Met Leu Leu His Leu Val
      115            120            125

Arg Gly Lys Val Lys Glu Phe Tyr Ser Tyr Glu Asn Glu Pro Val Gly
      130            135            140

Ile Glu Asn Leu Lys Arg Gly Leu Ala Ser Leu Phe Gln Met Gln Leu
      145            150            155            160

Ser Ser Gly Thr Thr Asn Glu Val Asp Ile Ser Gly Asp Cys Lys Val
      165            170            175

Thr Tyr Gln Ala Gln Gln Asp Lys Val Val Lys Ile Lys Ala Leu Asp
      180            185            190

Thr Cys Lys Ile Glu Arg Ser Gly Phe Thr Thr Ala Asn Gln Val Leu
      195            200            205

```

Gly Val Ser Ser Lys Ala Thr Ser Val Thr Thr Tyr Lys Ile Glu Asp
 210 215 220
 Ser Phe Val Thr Ala Val Leu Ala Glu Glu Thr Arg Ala Phe Ala Leu
 225 230 235 240
 Asn Phe Gln Gln Thr Ile Ala Gly Lys Ile Val Ser Lys Gln Lys Leu
 245 250 255
 Glu Leu Lys Thr Thr Glu Ala Gly Pro Arg Met Ile Pro Gly Lys Gln
 260 265 270
 Val Ala Gly Val Ile Lys Ala Val Asp Ser Lys Tyr Lys Ala Ile Pro
 275 280 285
 Ile Val Gly Gln Val Leu Glu Arg Val Cys Lys Gly Cys Pro Ser Leu
 290 295 300
 Ala Glu His Trp Lys Ser Ile Arg Lys Asn Leu Glu Pro Glu Asn Leu
 305 310 315 320
 Ser Lys Ala Glu Ala Val Gln Ser Phe Leu Ala Phe Ile Gln His Leu
 325 330 335
 Arg Thr Ser Arg Arg Glu Glu Ile Leu Gln Ile Leu Lys Ala Glu Lys
 340 345 350
 Lys Glu Val Leu Pro Gln Leu Val Asp Ala Val Thr Ser Ala Gln Thr
 355 360 365
 Pro Asp Ser Leu Glu Ala Ile Leu Asp Phe Leu Asp Phe Lys Ser Asp
 370 375 380
 Ser Ser Ile Ile Leu Gln Glu Arg Phe Leu Tyr Ala Cys Gly Phe Ala
 385 390 395 400
 Thr His Pro Asp Glu Glu Leu Leu Arg Ala Leu Leu Ser Lys Phe Lys
 405 410 415
 Gly Ser Phe Ala Ser Asn Asp Ile Arg Glu Ser Val Met Ile Ile Ile
 420 425 430
 Gly Ala Leu Val Arg Lys Leu Cys Gln Asn Glu Gly Cys Lys Leu Lys
 435 440 445
 Ala Val Val Glu Ala Lys Lys Leu Ile Leu Gly Gly Leu Glu Lys Pro
 450 455 460
 Glu Lys Lys Glu Asp Thr Thr Met Tyr Leu Leu Ala Leu Lys Asn Ala
 465 470 475 480
 Leu Leu Pro Glu Gly Ile Pro Leu Leu Lys Tyr Ala Glu Ala Gly
 485 490 495
 Glu Gly Pro Val Ser His Leu Ala Thr Thr Val Leu Gln Arg Tyr Asp
 500 505 510
 Val Ser Phe Ile Thr Asp Glu Val Lys Lys Thr Leu Asn Arg Ile Tyr
 515 520 525
 His Gln Asn Arg Lys Val His Glu Lys Thr Val Arg Thr Thr Ala Ala
 530 535 540

Ala Val Ile Leu Lys Asn Pro Ser Tyr Met Asp Val Lys Asn Ile Leu
 545 550 555 560
 Leu Ser Ile Gly Glu Leu Pro Lys Glu Met Asn Lys Tyr Met Leu Thr
 565 570 575
 Val Val Gln Asp Ile Leu His Phe Glu Met Pro Ala Ser Lys Met Ile
 580 585 590
 Arg Arg Val Leu Lys Glu Met Ala Val His Asn Tyr Asp Arg Phe Ser
 595 600 605
 Lys Ser Gly Ser Ser Ser Ala Tyr Thr Gly Tyr Val Glu Arg Ser Pro
 610 615 620
 Arg Ala Ala Ser Thr Tyr Ser Leu Asp Ile Leu Tyr Ser Gly Ser Gly
 625 630 635 640
 Ile Leu Arg Arg Ser Asn Leu Asn Ile Phe Gln Tyr Ile Lys Gly Thr
 645 650 655
 Glu Leu His Gly Ser Gln Val Val Ile Glu Ala Gln Gly Leu Glu Gly
 660 665 670
 Leu Ile Ala Ala Thr Pro Asp Glu Gly Glu Glu Asn Leu Asp Ser Tyr
 675 680 685
 Ala Gly Met Ser Ala Ile Leu Phe Asp Val Gln Leu Arg Pro Val Thr
 690 695 700
 Phe Phe Asn Gly Tyr Ser Asp Leu Met Ser Lys Met Leu Ser Ala Ser
 705 710 715 720
 Gly Asp Pro Val Ser Val Val Lys Gly Leu Ile Leu Leu Ile Asp His
 725 730 735
 Ser Gln Asp Ile Gln Leu Gln Ser Gly Leu Lys Ala Asn Met Glu Ile
 740 745 750
 Gln Gly Gly Leu Ala Ile Asp Ile Ser Gly Ser Met Glu Phe Ser Leu
 755 760 765
 Trp Tyr Arg Glu Ser Lys Thr Arg Val Lys Asn Arg Val Ala Val Val
 770 775 780
 Ile Thr Ser Asp Val Thr Val Asp Ala Ser Phe Val Lys Ala Gly Leu
 785 790 795 800
 Glu Ser Arg Ala Glu Thr Glu Ala Gly Leu Glu Phe Ile Ser Thr Val
 805 810 815
 Gln Phe Ser Gln Tyr Pro Phe Leu Val Cys Met Gln Met Asp Lys Ala
 820 825 830
 Glu Ala Pro Leu Arg Gln Phe Glu Thr Lys Tyr Glu Arg Leu Ser Thr
 835 840 845
 Gly Arg Gly Tyr Val Ser Arg Arg Arg Lys Glu Ser Leu Val Ala Gly
 850 855 860
 Cys Glu Leu Pro Leu His Gln Gln Asn Ser Glu Met Cys Asn Val Val
 865 870 875 880
 Phe Pro Pro Gln Pro Glu Ser Asp Asn Ser Gly Gly Trp Phe

<210> 7
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer

<400> 7
 ggagaaacgg tcataattgt g 21

<210> 8
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer

<400> 8
 gtgggcccgt ctaggcacca a 21

<210> 9
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer

<400> 9
 ctctttgatg tcacgcacga tttc 24

<210> 10
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer

<400> 10
 ggactttttg gatttcaaaa gtgac 25

<210> 11
 <211> 264
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)..(261)
 <223> Wherein Xaa is any amino acid.

```

<400> 11
Met Asp Pro Pro Arg Pro Ala Leu Leu Ala Leu Leu Ala Xaa Pro Xaa
1          5          10          15

Leu Leu Leu Leu Leu Leu Ala Gly Ala Arg Xaa Glu Glu Glu Xaa Leu
20          25          30

Glu Asn Val Xaa Leu Val Cys Pro Lys Asp Xaa Thr Arg Phe Xaa His
35          40          45

Leu Xaa Lys Xaa Xaa Tyr Asn Tyr Glu Ala Glu Ser Ser Ser Gly Val
50          55          60

Pro Gly Thr Ala Xaa Ser Arg Ser Ala Thr Arg Xaa Asn Cys Lys Xaa
65          70          75          80

Glu Leu Glu Val Pro Gln Leu Cys Ser Phe Ile Leu Lys Xaa Ser Gln
85          90          95

Cys Thr Leu Lys Glu Val Tyr Gly Phe Asn Pro Glu Gly Lys Ala Leu
100         105         110

Leu Lys Lys Thr Lys Asn Ser Xaa Glu Xaa Ala Ala Ala Met Ser Arg
115         120         125

Xaa Glu Leu Lys Leu Ala Ile Pro Glu Gly Lys Gln Val Phe Leu Tyr
130         135         140

Pro Glu Lys Asp Glu Pro Thr Tyr Ile Leu Asn Ile Lys Arg Gly Ile
145         150         155         160

Ile Ser Ala Leu Leu Val Pro Pro Glu Xaa Glu Glu Ala Lys Gln Xaa
165         170         175

Leu Phe Xaa Asp Thr Val Tyr Gly Asn Cys Ser Thr His Phe Thr Val
180         185         190

Lys Thr Arg Xaa Gly Asn Xaa Ala Thr Xaa Xaa Ser Thr Glu Arg Asp
195         200         205

Leu Gly Gln Cys Asp Arg Phe Lys Pro Ile Arg Thr Gly Ile Ser Pro
210         215         220

Xaa Ala Leu Ile Lys Gly Met Xaa Arg Pro Leu Ser Thr Leu Ile Xaa
225         230         235         240

Ser Xaa Gln Ser Cys Gln Xaa Thr Leu Asp Ala Lys Arg Lys His Val
245         250         255

Ala Glu Xaa Xaa Cys Lys Glu Gln
260

```

```

<210> 12
<211> 335
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)..(335)
<223> Wherein Xaa is any amino acid.

```

<400> 12

Met Gly Cys Leu Leu Phe Leu Leu Leu Trp Ala Leu Leu Gln Ala Trp
1 5 10 15
Gly Ser Ala Glu Val Pro Gln Arg Leu Phe Pro Leu Arg Cys Leu Gln
20 25 30
Xaa Ser Xaa Phe Ala Asn Ser Ser Trp Thr Arg Thr Asp Xaa Leu Ala
35 40 45
Trp Xaa Gly Glu Leu Gln Xaa His Ser Trp Ser Asn Asp Xaa Asp Thr
50 55 60
Val Xaa Ser Leu Xaa Pro Xaa Xaa Gln Gly Thr Phe Ser Asp Gln Gln
65 70 75 80
Trp Glu Thr Leu Gln His Ile Phe Arg Val Tyr Arg Ser Ser Phe Thr
85 90 95
Arg Asp Val Lys Xaa Phe Ala Lys Met Leu Arg Xaa Ser Tyr Pro Xaa
100 105 110
Glu Leu Gln Val Ser Ala Gly Cys Glu Val His Pro Gly Asn Ala Xaa
115 120 125
Asn Asn Phe Phe His Val Ala Phe Gln Gly Lys Asp Ile Leu Ser Phe
130 135 140
Gln Gly Thr Ser Trp Glu Pro Thr Gln Glu Ala Pro Leu Trp Val Asn
145 150 155 160
Leu Ala Ile Gln Val Leu Asn Gln Xaa Lys Xaa Thr Arg Glu Thr Val
165 170 175
Gln Xaa Leu Leu Asn Gly Thr Cys Pro Gln Phe Val Ser Gly Leu Leu
180 185 190
Glu Ser Gly Lys Ser Glu Leu Lys Lys Gln Val Lys Pro Lys Ala Trp
195 200 205
Leu Ser Arg Gly Pro Xaa Pro Gly Pro Gly Arg Xaa Leu Leu Xaa Cys
210 215 220
His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Lys Trp Met Xaa
225 230 235 240
Gly Glu Gln Glu Gln Gln Gly Thr Gln Pro Gly Asp Xaa Leu Pro Asn
245 250 255
Ala Asp Glu Thr Trp Tyr Leu Arg Ala Thr Leu Xaa Xaa Val Ala Gly
260 265 270
Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser Ser Leu Glu Gly
275 280 285
Gln Asp Xaa Val Leu Tyr Trp Gly Gly Xaa Tyr Thr Ser Met Gly Leu
290 295 300
Ile Xaa Leu Xaa Val Leu Ala Cys Leu Leu Phe Leu Leu Ile Val Gly
305 310 315 320
Xaa Thr Ser Arg Phe Lys Arg Gln Thr Ser Tyr Gln Xaa Xaa Leu
325 330 335

<210> 13
 <211> 210
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)..(210)
 <223> Wherein Xaa is any amino acid.

<400> 13
 Lys Cys Val Gln Ser Xaa Lys Pro Ser Leu Met Ile Gln Lys Ala Xaa
 1 5 10 15
 Xaa Gln Ala Leu Arg Lys Met Glu Pro Lys Asp Lys Asp Gln Glu Val
 20 25 30
 Leu Leu Gln Thr Phe Leu Asp Asp Ala Ser Pro Gly Asp Xaa Arg Xaa
 35 40 45
 Ala Ala Xaa Leu Met Xaa Xaa Arg Ser Pro Ser Gln Ala Asp Xaa Asn
 50 55 60
 Lys Ile Val Gln Xaa Leu Pro Trp Glu Gln Asn Glu Gln Val Lys Asn
 65 70 75 80
 Xaa Val Ala Xaa His Ile Ala Asn Xaa Leu Asn Ser Glu Glu Xaa Asp
 85 90 95
 Xaa Gln Asp Leu Lys Lys Leu Val Xaa Glu Ala Xaa Lys Glu Ser Gln
 100 105 110
 Leu Pro Thr Val Met Asp Phe Arg Lys Phe Ser Arg Asn Tyr Gln Leu
 115 120 125
 Tyr Lys Ser Val Xaa Leu Pro Ser Leu Asp Pro Xaa Ser Xaa Lys Ile
 130 135 140
 Glu Gly Asn Leu Xaa Phe Asp Pro Asn Asn Xaa Leu Pro Lys Glu Ser
 145 150 155 160
 Met Xaa Xaa Thr Thr Leu Thr Ala Phe Gly Phe Ala Ser Xaa Asp Xaa
 165 170 175
 Xaa Glu Ile Xaa Leu Glu Gly Lys Gly Phe Glu Pro Thr Leu Xaa Ala
 180 185 190
 Xaa Phe Gly Lys Gln Xaa Phe Phe Pro Xaa Ser Val Asn Lys Ala Leu
 195 200 205
 Tyr Trp
 210

<210> 14
 <211> 301
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)..(301)
 <223> Wherein Xaa is any amino acid.

<400> 14

Phe Ser Tyr Asn Asn Lys Tyr Gly Met Val Ala Gln Val Thr Gln Thr
1 5 10 15
Leu Lys Leu Glu Asp Thr Pro Lys Ile Asn Ser Arg Phe Phe Gly Glu
20 25 30
Gly Thr Xaa Lys Met Gly Leu Ala Xaa Glu Ser Thr Lys Ser Thr Ser
35 40 45
Pro Pro Lys Xaa Ala Glu Ala Val Xaa Xaa Xaa Leu Gln Glu Leu Lys
50 55 60
Lys Leu Thr Ile Ser Xaa Gln Xaa Ile Gln Arg Ala Xaa Leu Phe Asn
65 70 75 80
Xaa Xaa Val Thr Glu Leu Arg Gly Leu Ser Asp Glu Ala Val Thr Ser
85 90 95
Xaa Leu Pro Gln Leu Ile Glu Xaa Ser Ser Pro Xaa Xaa Leu Gln Ala
100 105 110
Leu Val Gln Cys Gly Xaa Pro Gln Cys Ser Thr His Ile Xaa Gln Xaa
115 120 125
Leu Lys Xaa Val His Ala Asn Pro Leu Leu Ile Asp Val Val Thr Tyr
130 135 140
Leu Val Ala Leu Xaa Pro Glu Pro Ser Ala Gln Gln Xaa Arg Glu Ile
145 150 155 160
Phe Asn Met Ala Arg Xaa Gln Arg Ser Arg Ala Thr Leu Tyr Ala Leu
165 170 175
Ser His Ala Val Asn Asn Tyr His Lys Xaa Asn Pro Xaa Gly Thr Gln
180 185 190
Glu Leu Xaa Asp Ile Ala Asn Xaa Leu Met Glu Gln Ile Gln Asp Asp
195 200 205
Cys Xaa Gly Asp Glu Asp Tyr Thr Tyr Leu Xaa Leu Arg Xaa Ile Gly
210 215 220
Asn Met Gly Gln Thr Met Glu Gln Leu Thr Pro Glu Leu Lys Ser Xaa
225 230 235 240
Ile Leu Lys Cys Val Gln Ser Thr Lys Pro Ser Xaa Xaa Ile Gln Lys
245 250 255
Ala Ala Ile Gln Xaa Leu Arg Lys Met Glu Pro Lys Asp Lys Asp Gln
260 265 270
Xaa Xaa Xaa Leu Gln Thr Phe Leu Asp Asp Ala Ser Pro Gly Asp Lys
275 280 285
Arg Leu Ala Ala Tyr Leu Met Leu Xaa Arg Ser Pro Ser
290 295 300

<210> 15

<211> 335

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)..(335)

<223> Wherein Xaa is any amino acid.

<400> 15

Met Gly Cys Leu Leu Phe Leu Leu Leu Trp Ala Leu Leu Gln Ala Trp
1 5 10 15

Gly Ser Ala Glu Val Pro Gln Arg Leu Phe Pro Leu Arg Cys Leu Gln
20 25 30

Ile Ser Ser Phe Ala Asn Ser Ser Trp Thr Arg Thr Asp Gly Leu Ala
35 40 45

Trp Leu Gly Glu Leu Gln Thr His Xaa Trp Ser Asn Asp Ser Asp Thr
50 55 60

Val Arg Xaa Xaa Lys Pro Trp Ser Gln Gly Thr Phe Ser Asp Gln Gln
65 70 75 80

Trp Glu Thr Leu Gln His Ile Phe Arg Val Tyr Arg Ser Ser Phe Thr
85 90 95

Xaa Asp Xaa Lys Glu Xaa Ala Lys Xaa Xaa Arg Leu Ser Tyr Pro Leu
100 105 110

Glu Leu Gln Xaa Ser Ala Gly Cys Glu Xaa His Pro Gly Asn Ala Ser
115 120 125

Asn Asn Phe Phe His Val Ala Phe Gln Gly Lys Asp Ile Leu Ser Phe
130 135 140

Gln Gly Thr Ser Xaa Glu Pro Xaa Gln Glu Ala Pro Xaa Trp Val Asn
145 150 155 160

Leu Ala Xaa Gln Xaa Leu Asn Gln Asp Lys Trp Thr Xaa Glu Thr Xaa
165 170 175

Gln Trp Leu Leu Asn Gly Thr Cys Pro Gln Phe Val Ser Gly Leu Leu
180 185 190

Glu Ser Gly Lys Ser Glu Leu Lys Lys Gln Val Lys Pro Lys Xaa Trp
195 200 205

Leu Ser Arg Gly Pro Xaa Pro Xaa Pro Gly Arg Leu Leu Leu Xaa Cys
210 215 220

His Val Ser Gly Xaa Tyr Pro Lys Pro Val Trp Val Lys Trp Xaa Xaa
225 230 235 240

Gly Glu Gln Glu Gln Gln Gly Thr Gln Pro Xaa Asp Xaa Xaa Pro Asn
245 250 255

Xaa Asp Glu Thr Trp Tyr Leu Arg Ala Thr Leu Xaa Val Xaa Ala Gly
260 265 270

Glu Ala Xaa Gly Leu Ser Cys Arg Val Lys His Ser Ser Leu Xaa Gly
275 280 285

Gln Asp Ile Val Leu Tyr Trp Gly Gly Ser Tyr Thr Ser Met Gly Leu
290 295 300

Ile Ala Leu Ala Val Leu Ala Cys Leu Leu Phe Leu Leu Ile Val Gly
 305 310 315 320

Phe Thr Ser Arg Phe Lys Arg Gln Thr Ser Tyr Gln Gly Val Leu
 325 330 335

<210> 16
 <211> 335
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)..(335)
 <223> Wherein Xaa is any amino acid.

<400> 16
 Met Gly Cys Leu Leu Phe Leu Leu Leu Trp Ala Leu Leu Gln Ala Trp
 1 5 10 15

Gly Ser Ala Glu Val Pro Gln Arg Leu Phe Pro Leu Arg Cys Leu Gln
 20 25 30

Ile Ser Ser Phe Ala Asn Ser Ser Trp Thr Xaa Thr Asp Gly Leu Ala
 35 40 45

Xaa Leu Gly Glu Leu Gln Thr His Ser Trp Ser Xaa Asp Ser Asp Thr
 50 55 60

Xaa Xaa Xaa Leu Lys Pro Trp Ser Gln Gly Thr Phe Ser Xaa Gln Xaa
 65 70 75 80

Trp Glu Thr Leu Xaa His Ile Phe Xaa Xaa Tyr Arg Ser Ser Phe Thr
 85 90 95

Arg Asp Val Lys Glu Phe Ala Lys Xaa Leu Arg Leu Ser Tyr Pro Xaa
 100 105 110

Glu Leu Gln Xaa Xaa Ala Gly Cys Glu Val His Pro Gly Xaa Ala Ser
 115 120 125

Asn Asn Phe Phe His Xaa Ala Xaa Gln Gly Xaa Asp Ile Leu Ser Phe
 130 135 140

Gln Gly Thr Ser Trp Glu Pro Thr Gln Glu Ala Pro Xaa Trp Val Asn
 145 150 155 160

Leu Ala Ile Gln Xaa Leu Asn Gln Asp Lys Trp Thr Arg Xaa Thr Val
 165 170 175

Gln Trp Leu Leu Asn Gly Thr Cys Pro Gln Phe Val Ser Gly Leu Leu
 180 185 190

Glu Xaa Gly Lys Xaa Glu Leu Lys Lys Gln Xaa Lys Pro Lys Ala Xaa
 195 200 205

Leu Ser Arg Gly Pro Ser Pro Gly Pro Gly Arg Leu Leu Leu Val Cys
 210 215 220

His Val Xaa Gly Phe Tyr Pro Lys Pro Val Trp Xaa Lys Trp Xaa Arg
 225 230 235 240

Gly Glu Gln Glu Gln Gln Gly Thr Gln Pro Gly Asp Ile Leu Pro Asn

				245					250					255		
Xaa	Asp	Glu	Thr	Trp	Tyr	Leu	Arg	Ala	Thr	Leu	Asp	Xaa	Xaa	Ala	Gly	
			260					265					270			
Glu	Ala	Ala	Gly	Leu	Xaa	Cys	Arg	Val	Lys	His	Ser	Ser	Leu	Glu	Gly	
		275					280					285				
Gln	Xaa	Xaa	Xaa	Leu	Tyr	Trp	Gly	Gly	Ser	Tyr	Thr	Ser	Met	Gly	Leu	
	290					295					300					
Ile	Ala	Leu	Ala	Val	Leu	Ala	Cys	Leu	Xaa	Phe	Leu	Leu	Ile	Val	Gly	
305					310					315					320	
Phe	Thr	Ser	Arg	Phe	Lys	Arg	Gln	Thr	Ser	Tyr	Gln	Gly	Val	Leu		
				325					330					335		